

SEQUENCE LISTING

<110> Daniel E. Afar
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Douglas C. Saffran

<120> NOVEL TUMOR ANTIGEN USEFUL IN DIAGNOSIS
AND THERAPY OF PROSTATE AND COLON CANCER

<130> 129.8USU1

<140> 09/323,597

<141> 1999-06-01

<150> 60/087,598

<151> 1998-06-01

<150> 60/091,474

<151> 1998-06-29

<150> 60/129,521

<151> 1999-04-14

<160> 13

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<211> 1738

<212> DNA

<213> Homo sapiens

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ttg aac tca ggg tca cca cca gct att gga cct tac tat gaa aac cat 165
Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn His
5 10 15

gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc ccc 213
Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val Pro
20 25 30

act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg ccc 261
Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val Pro
35 40 45 50

cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc tgc 309
Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val Cys
55 60 65

acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act aag 357

Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr Lys
 70 75 80

aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga gct 405
 Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly Ala
 85 90 95

gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc tcc 453
 Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys Ser
 100 105 110

aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc tct 501
 Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro Ser
 115 120 125 130

aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag aat 549
 Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn
 135 140 145

cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag gtg tac tca 597
 Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val Tyr Ser
 150 155 160

tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac gag 645
 Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn Glu
 165 170 175

aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat ttt 693
 Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn Phe
 180 185 190

tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt atg 741
 Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe Met
 195 200 205 210

aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg tac 789
 Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu Tyr
 215 220 225

cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt ata 837
 His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys Ile
 230 235 240

gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg att gtg ggc 885
 Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val Gly
 245 250 255

ggc gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg cac 933
 Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu His
 260 265 270

gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag tgg 981
 Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu Trp
 275 280 285 290

atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca tgg 1029
 Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro Trp
 295 300 305

cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc tat 1077
 His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe Tyr
 310 315 320

gga gcc gga tac caa gta gaa aaa gtg att tct cat cca aat tat gac 1125
 Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn Tyr Asp
 325 330 335

tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag cct 1173
 Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys Pro
 340 345 350

ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca ggc 1221
 Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro Gly
 355 360 365 370

atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg gcc 1269
 Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly Ala
 375 380 385

acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag gtg 1317
 Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys Val
 390 395 400

ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac aac 1365
 Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp Asn
 405 410 415

ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac gtc 1413
 Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn Val
 420 425 430

gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tcg aag aac 1461
 Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Lys Asn
 435 440 445 450

aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt gcc 1509
 Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly Cys Ala
 455 460 465

aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg gac 1557
 Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr Asp
 470 475 480

tgg att tat cga caa atg agg gca gac ggc t aatccacatg gtcttcgtcc 1608
 Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly
 485 490

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 aaaaaaaaaa 1738

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<211> 492

<212> PRT

<213> Homo sapiens

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 35 40 45
 Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 50 55 60
 Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys

65 70 75 80
 Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
 85 90 95
 Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
 100 105 110
 Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
 115 120 125
 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
 130 135 140
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val
 145 150 155 160
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
 165 170 175
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
 180 185 190
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
 195 200 205
 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
 210 215 220
 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
 225 230 235 240
 Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
 245 250 255
 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
 260 265 270
 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
 275 280 285
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
 290 295 300
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
 305 310 315 320
 Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn
 325 330 335
 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
 340 345 350
 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
 355 360 365
 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
 370 375 380
 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
 385 390 395 400
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
 405 410 415
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
 420 425 430
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
 435 440 445
 Lys Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
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cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc	155



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ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg 203
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tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act 299
aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga 347
gct gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc 395
tcc aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc 443
tct aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag 491
aat cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag atg tac 539
tca tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac 587
gag aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat 635
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atg aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg 731
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tat gga gcc gga tac caa gta caa aaa gtg att tct cat cca aat tat 1067
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cct ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca 1163
ggc atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg 1211
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gtg ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac 1307
aac ctg atc aca cca gcc atg atc tgc gcc ggc ttc ctg cag ggg aac 1355
gtc gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tgc aac 1403
aac aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt 1451
gcc aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg 1499
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<210> 4
<211> 492
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Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
          35          40          45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
          50          55          60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
          65          70          75          80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val

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85 90 95
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 Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
 130 135 140
 Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
 145 150 155 160
 Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
 165 170 175
 Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
 180 185 190
 Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
 195 200 205
 Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
 210 215 220
 Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
 225 230 235 240
 Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
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 Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
 260 265 270
 Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
 275 280 285
 Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
 290 295 300
 Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
 305 310 315 320
 Phe Tyr Gly Ala Gly Tyr Gln Val Gln Lys Val Ile Ser His Pro Asn
 325 330 335
 Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
 340 345 350
 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
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<223> cDNA Synthesis Primer

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<210> 7

<211> 44

<212> DNA

<213> Artificial Sequence

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<210> 8

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<223> DNA Adaptor 2

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<212> DNA

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<212> DNA

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